

Edward H Snell

List of Publications by Year in descending order

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97
papers

2,486
citations

186265

28
h-index

233421

45
g-index

102
all docs

102
docs citations

102
times ranked

3031
citing authors

#	ARTICLE	IF	CITATIONS
1	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1212-1231.	2.6	3
2	Microgravity as an environment for macromolecular crystallization – an outlook in the era of space stations and commercial space flight. <i>Crystallography Reviews</i> , 2021, 27, 3-46.	1.5	11
3	Structural biology in the time of COVID-19: perspectives on methods and milestones. <i>IUCr</i> , 2021, 8, 335-341.	2.2	14
4	Near-physiological-temperature serial crystallography reveals conformations of SARS-CoV-2 main protease active site for improved drug repurposing. <i>Structure</i> , 2021, 29, 1382-1396.e6.	3.3	28
5	A SAXS-based approach to rationally evaluate radical scavengers – toward eliminating radiation damage in solution and crystallographic studies. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 1309-1320.	2.4	4
6	High-Throughput PIXE as an Essential Quantitative Assay for Accurate Metalloprotein Structural Analysis: Development and Application. <i>Journal of the American Chemical Society</i> , 2020, 142, 185-197.	13.7	24
7	Structural insights into conformational switching in latency-associated peptide between transforming growth factor β -1 bound and unbound states. <i>IUCr</i> , 2020, 7, 238-252.	2.2	5
8	SAXS studies of X-ray induced disulfide bond damage: Engineering high-resolution insight from a low-resolution technique. <i>PLoS ONE</i> , 2020, 15, e0239702.	2.5	9
9	Protein and RNA dynamical fingerprinting. <i>Nature Communications</i> , 2019, 10, 1026.	12.8	72
10	Structural knowledge or X-ray damage? A case study on xylose isomerase illustrating both. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 931-944.	2.4	12
11	Structural consequences of transforming growth factor beta-1 activation from near-therapeutic X-ray doses. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 967-979.	2.4	10
12	Classification of crystallization outcomes using deep convolutional neural networks. <i>PLoS ONE</i> , 2018, 13, e0198883.	2.5	54
13	Importance of Protein Vibration Directionality on Function. <i>Biophysical Journal</i> , 2017, 112, 353a.	0.5	0
14	FRET, SAXS and Molecular Simulations Resolve the Solution Structures of Three Coexisting Conformers of Flexible RNA Four-Way Junction. <i>Biophysical Journal</i> , 2017, 112, 367a.	0.5	0
15	Moving in the Right Direction: Protein Vibrations Steering Function. <i>Biophysical Journal</i> , 2017, 112, 933-942.	0.5	50
16	Double-flow focused liquid injector for efficient serial femtosecond crystallography. <i>Scientific Reports</i> , 2017, 7, 44628.	3.3	90
17	Anisotropic absorption measurements reveal protein dynamical transition in intramolecular vibrations. , 2016, , .		0
18	Computational crystallization. <i>Archives of Biochemistry and Biophysics</i> , 2016, 602, 12-20.	3.0	12

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19	Optical Absorbance Sensitivity to Rugged Energy Landscape. <i>Biophysical Journal</i> , 2016, 110, 513a.	0.5	0
20	The Effect of the Protein Dynamical Transition on Intramolecular Vibrations. <i>Biophysical Journal</i> , 2016, 110, 222a.	0.5	0
21	The use of haptic interfaces and web services in crystallography: an application for a 'screen to beam' interface. <i>Journal of Applied Crystallography</i> , 2016, 49, 2082-2090.	4.5	1
22	Long-Range Protein Vibrations Dependence on Ligand Binding: Rate Promoting Motions. <i>Biophysical Journal</i> , 2015, 108, 61a.	0.5	0
23	The detection and subsequent volume optimization of biological nanocrystals. <i>Structural Dynamics</i> , 2015, 2, 041710.	2.3	5
24	The accurate assessment of small-angle X-ray scattering data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 45-56.	2.5	34
25	A hybrid NMR/SAXS-based approach for discriminating oligomeric protein interfaces using $\langle \text{scp} \rangle$ osetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 309-317.	2.6	33
26	The Structure of the PanD/PanZ Protein Complex Reveals Negative Feedback Regulation of Pantothenate Biosynthesis by Coenzyme A. <i>Chemistry and Biology</i> , 2015, 22, 492-503.	6.0	30
27	Statistical Analysis of Crystallization Database Links Protein Physico-Chemical Features with Crystallization Mechanisms. <i>PLoS ONE</i> , 2014, 9, e101123.	2.5	18
28	Neutron structure of the cyclic glucose-bound xylose isomerase E186Q mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 414-420.	2.5	17
29	Measurements and calculations of protein intramolecular vibrations in the THz range. , 2014, , .		3
30	Crystallization screening: the influence of history on current practice. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 835-853.	0.8	54
31	Optical measurements of long-range protein vibrations. <i>Nature Communications</i> , 2014, 5, 3076.	12.8	166
32	Identifying, studying and making good use of macromolecular crystals. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 993-1008.	0.8	23
33	Long-Range Correlated Motion Changes with Protein-Ligand Binding. <i>Biophysical Journal</i> , 2014, 106, 237a.	0.5	1
34	A new view on crystal harvesting. <i>Journal of Applied Crystallography</i> , 2014, 47, 1158-1161.	4.5	2
35	Comparing Chemistry to Outcome: The Development of a Chemical Distance Metric, Coupled with Clustering and Hierarchal Visualization Applied to Macromolecular Crystallography. <i>PLoS ONE</i> , 2014, 9, e100782.	2.5	14
36	The Structure of Yeast GlutaminyI-tRNA Synthetase and Modeling of Its Interaction with tRNA. <i>Journal of Molecular Biology</i> , 2013, 425, 2480-2493.	4.2	13

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37	Correlated Motions in Protein Crystals Measured by THz Microscopy. <i>Biophysical Journal</i> , 2013, 104, 555a.	0.5	0
38	Measuring phonons in protein crystals. <i>Proceedings of SPIE</i> , 2013, , .	0.8	0
39	Insights into the mechanism of X-ray-induced disulfide-bond cleavage in lysozyme crystals based on EPR, optical absorption and X-ray diffraction studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2381-2394.	2.5	51
40	THz microscopy measurements on inhibitor dependence of protein intramolecular modes. , 2013, , .		2
41	Purification and SAXS Analysis of the Integrin Linked Kinase, PINCH, Parvin (IPP) Heterotrimeric Complex. <i>PLoS ONE</i> , 2013, 8, e55591.	2.5	12
42	Structural conservation of an ancient tRNA sensor in eukaryotic glutamyl-tRNA synthetase. <i>Nucleic Acids Research</i> , 2012, 40, 3723-3731.	14.5	14
43	Orientation sensitive Terahertz resonances observed in protein crystals. , 2012, , .		3
44	On the need for an international effort to capture, share and use crystallization screening data. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 253-258.	0.7	38
45	Whatâ€™s in a Drop? Correlating Observations and Outcomes to Guide Macromolecular Crystallization Experiments. <i>Crystal Growth and Design</i> , 2011, 11, 651-663.	3.0	52
46	Lessons from high-throughput protein crystallization screening: 10 years of practical experience. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 465-480.	5.0	43
47	Small angle X-ray scattering as a complementary tool for high-throughput structural studies. <i>Biopolymers</i> , 2011, 95, 517-530.	2.4	69
48	Crystal cookery â€“ using high-throughput technologies and the grocery store as a teaching tool. <i>Journal of Applied Crystallography</i> , 2010, 43, 1189-1207.	4.5	7
49	Sliding Clampâ€™DNA Interactions Are Required for Viability and Contribute to DNA Polymerase Management in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2009, 387, 74-91.	4.2	39
50	Glycerol concentrations required for the successful vitrification of cocktail conditions in a high-throughput crystallization screen. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 287-301.	2.5	8
51	Establishing a training set through the visual analysis of crystallization trials. Part I: 1/4150â€™...000 images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1123-1130.	2.5	25
52	Establishing a training set through the visual analysis of crystallization trials. Part II: crystal examples. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1131-1137.	2.5	18
53	The application and use of chemical space mapping to interpret crystallization screening results. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1240-1249.	2.5	26
54	<i>AutoSherlock</i>: a program for effective crystallization data analysis. <i>Journal of Applied Crystallography</i> , 2008, 41, 1173-1176.	4.5	14

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55	Structure of the Full-length Human RPA14/32 Complex Gives Insights into the Mechanism of DNA Binding and Complex Formation. <i>Journal of Molecular Biology</i> , 2007, 374, 865-876.	4.2	45
56	Changes to crystals of <i>Escherichia coli</i> β -galactosidase during room-temperature/low-temperature cycling and their relation to cryo-annealing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1139-1153.	2.5	12
57	Non-invasive measurement of X-ray beam heating on a surrogate crystal sample. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 109-115.	2.4	50
58	Efficient optimization of crystallization conditions by manipulation of drop volume ratio and temperature. <i>Protein Science</i> , 2007, 16, 715-722.	7.6	36
59	A quasi-Laue neutron crystallographic study of d-xylose isomerase. <i>European Biophysics Journal</i> , 2006, 35, 601-609.	2.2	28
60	Optimizing crystal volume for neutron diffraction: D-xylose isomerase. <i>European Biophysics Journal</i> , 2006, 35, 621-632.	2.2	12
61	Investigating the role of the <i>E. coli</i> β -sliding clamp in DNA polymerase β -dependent translesion DNA synthesis. <i>FASEB Journal</i> , 2006, 20, A909.	0.5	0
62	Extracting trends from two decades of microgravity macromolecular crystallization history. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 763-771.	2.5	24
63	Finding a cold needle in a warm haystack: infrared imaging applied to locating cryocooled crystals in loops. <i>Journal of Applied Crystallography</i> , 2005, 38, 69-77.	4.5	10
64	Macromolecular crystallization in microgravity. <i>Reports on Progress in Physics</i> , 2005, 68, 799-853.	20.1	83
65	Imaging modulated reflections from a semi-crystalline state of profilin:actin crystals. <i>Journal of Applied Crystallography</i> , 2004, 37, 327-330.	4.5	4
66	First results of digital topography applied to macromolecular crystals. <i>Journal of Applied Crystallography</i> , 2004, 37, 481-485.	4.5	9
67	Physical and structural studies on the cryocooling of insulin crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2169-2182.	2.5	10
68	Macromolecular Crystal Quality. <i>Methods in Enzymology</i> , 2003, 368, 268-288.	1.0	15
69	The development and application of a method to quantify the quality of cryoprotectant solutions using standard area-detector X-ray images. <i>Journal of Applied Crystallography</i> , 2002, 35, 538-545.	4.5	42
70	Thaumatococcus crystallization aboard the International Space Station using liquid-liquid diffusion in the Enhanced Gaseous Nitrogen Dewar (EGN). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 751-760.	2.5	14
71	Seeing the heat – preliminary studies of cryocrystallography using infrared imaging. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 361-367.	2.4	14
72	Free-falling Crystals: Biological Macromolecular Crystal Growth Studies in Low Earth Orbit. <i>Asia-Pacific Journal of Chemical Engineering</i> , 2002, 10, 491-500.	0.0	1

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73	Microgravity and Macromolecular Crystallography. <i>Crystal Growth and Design</i> , 2001, 1, 87-99.	3.0	109
74	Investigating the Effect of Impurities on Macromolecule Crystal Growth in Microgravity. <i>Crystal Growth and Design</i> , 2001, 1, 151-158.	3.0	40
75	A test of macromolecular crystallization in microgravity: large well ordered insulin crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1204-1207.	2.5	32
76	BEAM-ish: a graphical user interface for the physical characterization of macromolecular crystals. <i>Journal of Applied Crystallography</i> , 2000, 33, 1187-1188.	4.5	11
77	Synchrotron X-ray reciprocal-space mapping, topography and diffraction resolution studies of macromolecular crystal quality. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 868-880.	2.5	59
78	The high-mosaicity illusion: revealing the true physical characteristics of macromolecular crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 986-995.	2.5	25
79	Cryo-trapping the six-coordinate, distorted-octahedral active site of manganese superoxide dismutase 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 296, 951-959.	4.2	77
80	Crystallization of chicken egg white lysozyme from assorted sulfate salts. <i>Journal of Crystal Growth</i> , 1999, 196, 332-343.	1.5	31
81	The Effect of Temperature and Solution pH on the Nucleation of Tetragonal Lysozyme Crystals. <i>Biophysical Journal</i> , 1999, 77, 1585-1593.	0.5	104
82	Stationary Crystal Diffraction with a Monochromatic Convergent X-ray Source and Application for Macromolecular Crystal Data Collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 200-214.	2.5	11
83	Protein crystal movements and fluid flows during microgravity growth. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 1998, 356, 1045-1061.	3.4	17
84	CCD video observation of microgravity crystallization: apocrustacyanin C1. <i>Journal of Crystal Growth</i> , 1997, 171, 219-225.	1.5	54
85	Partial Improvement of Crystal Quality for Microgravity-Grown Apocrustacyanin C1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 231-239.	2.5	20
86	Crystallization of chicken egg-white lysozyme from ammonium sulfate. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 795-797.	2.5	19
87	CCD Video Observation of Microgravity Crystallization of Lysozyme and Correlation with Accelerometer Data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 747-755.	2.5	12
88	Partial improvement of crystal quality for microgravity-grown apocrustacyanin C1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 231-9.	2.5	0
89	Trends and Challenges in Experimental Macromolecular Crystallography. <i>Quarterly Reviews of Biophysics</i> , 1996, 29, 227-278.	5.7	72
90	Protein crystal perfection and the crystal growth process. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1996, 52, C517-C517.	0.3	0

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91	An investigation of the perfection of lysozyme protein crystals grown in microgravity and on earth. , 1996, , 155-170.		2
92	Lysozyme Crystal Growth Kinetics Monitored Using a MachéZehnder Interferometer. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 529-533.	2.5	14
93	The Daresbury Laboratory Laue Software Suite. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C50-C50.	0.3	1
94	Time-resolved biological and perturbation chemical crystallography: Laue and monochromatic developments. , 1995, , .		1
95	Improvements in lysozyme protein crystal perfection through microgravity growth. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 1099-1102.	2.5	86
96	Image-Plate Synchrotron Laue Data Collection and Subsequent Structural Analysis of a Small Test Crystal of a Nickel-Containing Aluminophosphate. Journal of Synchrotron Radiation, 1995, 2, 22-26.	2.4	0
97	Electron density maps of lysozyme calculated using synchrotron laue data comprising singles and deconvoluted multiples. Bulletin of Materials Science, 1994, 17, 1-18.	1.7	6